

Paper No. 9

1653
ENTERED MAR 12 2002 RECEIVEDDATE: 02/28/2002
TIME: 13:26:09RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/817,487AInput Set : A:\Sequence Listing.ST25.txt
Output Set: N:\CRF3\02282002\I817487A.raw

3 <110> APPLICANT: Novartis AG
 5 <120> TITLE OF INVENTION: Selectable Marker Genes
 7 <130> FILE REFERENCE: 4-31193A
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/817,487A
 C--> 9 <141> CURRENT FILING DATE: 2002-02-14
 9 <160> NUMBER OF SEQ ID NOS: 10
 11 <170> SOFTWARE: PatentIn version 3.0
 13 <210> SEQ ID NO: 1
 14 <211> LENGTH: 2607
 15 <212> TYPE: DNA
 16 <213> ORGANISM: homo sapiens
 18 <400> SEQUENCE: 1

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23 gttgaagaag tggctacttt catgtgtgca gtggaaatcct acccccagcc tgagatttcc	180
25 tggactagaa ataaaattct cattaaactc tttgacaccc ggtacagcat ccgggagaat	240
27 gggcagctcc tcaccatcct gagtgtggaa gacagtgtat atggcattta ctgctgcacg	300
29 gccaacaatg gtgtgggagg agctgtggag agttgtggag ccctgcaagt gaagatgaaa	360
31 cctaaaataa ctcgtcctcc cataaatgtg aaaataatag agggattaaa agcagtccct	420
33 ccatgtacta caatggtaa tcccaaaccac tcagtgctt ggataaaggg agacagccct	480
35 ctcaggaaat attccgaat tgcagttctt gaatctggga gcttgaggat tcataacgta	540
37 caaaaggaag atgcaggaca gtatcgatgt gtggaaaaaa acagcctcg gacagcatat	600
39 tccaaagtgg tgaagctgga atttgaggtt tttgccagga tcctgcggc tcctgaatcc	660
41 cacaatgtca ccttggctc ctttgtgacc ctgcactgta cagcaacagg cattcctgtc	720
43 cccaccatca cctggattga aaacggaaat gctgtttctt ctgggtccat tcaagagagt	780
45 gtgaaagacc gagtgattga ctcaagactg cagctgttta tcaccaagcc aggactctac	840
47 acatgcatac ctaccaataa gcatggggag aagttcagta ctgccaaggc tgcagccacc	900
49 atcagcatag cagaatggag taaaccacag aaagataaca aaggctactg cgcccagtac	960
51 agaggggagg tgtgtaatgc agtcctggca aaagatgctc ttgttttctt caacacctcc	1020
53 tatcgccacc ctgaggaggc ccaagagcta ctggccaca cggcctggaa tgaactgaaa	1080
55 gtatgtgacc cagtctgccc gccagctgtc gaggcttgc tttgttaaccatcttccat	1140
57 gagtgcagtc ctggagtagt gcctactcctt attccattt gcagagagta ctgcttggca	1200
59 gtaaaggagc tcttctgcgc aaaagaatgg ctggtaatgg aagagaagac ccacagagga	1260
61 ctctacagat ccgagatgca tttgtgtcc gtgcggaaat gcagcaagct tcccacatg	1320
63 cattgggacc ccacggcctg tgccagactg ccacatcttag attataacaa agaaaaccta	1380
65 aaaacattcc caccaatgac gtcctcaaag ccaagtgtgg acattccaa tctgccttcc	1440
67 tcctccttctt ctgccttc tttgtgtcc acataacttca tgactgtat aatctccatc	1500
69 atgtccagct ttgcaatatt tttgtgtcc accataacta ctgccttattt ctgcccggaa	1560
71 agaaaacaat gaaaaataa gaaaagagaa tcagcagcag taaccctcac cacactgcct	1620
73 tctgagctct tactagatag acttcatccc aacccatgt accagaggat gccgccttcc	1680
75 ctgaacccca aattgtcag ctggagtagt ccaaggata acattgtat tttgtgagagac	1740
77 atcggagagg gagcgttgg aagggtgtttt caagcaaggg caccaggctt acttccttat	1800
79 gaacctttca ctatggtggc agttaagatg ctcaaaaggaa aagcctcgcc agatatgca	1860

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81	gcggacttc	agagggaggc	agccctcatg	gcagaatttg	acaaccctaa	cattgtgaag	1920										
83	ctatttaggag	tgtgtgctgt	cgggaagcca	atgtgcctgc	tctttaata	catggcctat	1980										
85	ggtgaccta	atgagttcct	ccgcagcatg	tcccctcaca	ccgtgtcgag	cctcagtac	2040										
87	agtgacttgt	ctatgagggc	tcaggtctcc	agccctgggc	ccccaccctt	ctccgtgtct	2100										
89	gagcagctt	gcattgccag	gcaggtggca	gctggcatgg	cttacctctc	agaacgtaag	2160										
91	tttggtcacc	gagatttagc	caccaggaac	tgcctgggtgg	gcgagaacat	ggtgtgaaa	2220										
93	attgccgact	ttggcctctc	caggaacatc	tactcagcag	actactacaa	agctaataatgaa	2280										
95	aacgacgcta	tccctatccg	ttggatggca	ccagagtcca	ttttttataaa	ccgctacact	2340										
97	acagagtctg	atgtgtgggc	ctatggcggt	gtcctctggg	agatcttctc	ctatggcctg	2400										
99	cagccctact	atggatggc	ccatgaggag	gtcatttact	acgtgcgaga	tggcaacatc	2460										
101	ctctcctgcc	ctgagaactg	ccccgtggag	ctgtacaatc	tcatgcgtct	atgttggagc	2520										
103	aagctgcctg	cagacagacc	cagtttcacc	agtattcacc	gaattctgga	acgcatgtgt	2580										
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111	<213>	ORGANISM:	homo sapiens														
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116	1			5				10				15					
118	Ala	Phe	Ser	Gly	Thr	Glu	Lys	Leu	Pro	Lys	Ala	Pro	Val	Ile	Thr	Thr	
119				20				25				30					
121	Pro	Leu	Glu	Thr	Val	Asp	Ala	Leu	Val	Glu	Glu	Val	Ala	Thr	Phe	Met	
122				35				40				45					
124	Cys	Ala	Val	Glu	Ser	Tyr	Pro	Gln	Pro	Glu	Ile	Ser	Trp	Thr	Arg	Asn	
125				50				55				60					
127	Lys	Ile	Leu	Ile	Lys	Leu	Phe	Asp	Thr	Arg	Tyr	Ser	Ile	Arg	Glu	Asn	
128				65				70			75			80			
130	Gly	Gln	Leu	Leu	Thr	Ile	Leu	Ser	Val	Glu	Asp	Ser	Asp	Asp	Gly	Ile	
131					85				90				95				
133	Tyr	Cys	Cys	Thr	Ala	Asn	Asn	Gly	Val	Gly	Gly	Ala	Val	Glu	Ser	Cys	
134					100				105				110				
136	Gly	Ala	Leu	Gln	Val	Lys	Met	Lys	Pro	Lys	Ile	Thr	Arg	Pro	Pro	Ile	
137					115				120				125				
139	Asn	Val	Lys	Ile	Ile	Glu	Gly	Leu	Lys	Ala	Val	Leu	Pro	Cys	Thr	Thr	
140				130				135				140					
142	Met	Gly	Asn	Pro	Lys	Pro	Ser	Val	Ser	Trp	Ile	Lys	Gly	Asp	Ser	Pro	
143				145				150				155			160		
145	Leu	Arg	Glu	Asn	Ser	Arg	Ile	Ala	Val	Leu	Glu	Ser	Gly	Ser	Leu	Arg	
146					165				170				175				
148	Ile	His	Asn	Val	Gln	Lys	Glu	Asp	Ala	Gly	Gln	Tyr	Arg	Cys	Val	Ala	
149					180				185				190				
151	Lys	Asn	Ser	Leu	Gly	Thr	Ala	Tyr	Ser	Lys	Val	Val	Lys	Leu	Glu	Phe	
152				195				200				205					
154	Glu	Val	Phe	Ala	Arg	Ile	Leu	Arg	Ala	Pro	Glu	Ser	His	Asn	Val	Thr	
155				210				215				220					
157	Phe	Gly	Ser	Phe	Val	Thr	Leu	His	Cys	Thr	Ala	Thr	Gly	Ile	Pro	Val	
158				225				230				235			240		
160	Pro	Thr	Ile	Thr	Trp	Ile	Glu	Asn	Gly	Asn	Ala	Val	Ser	Ser	Gly	Ser	

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161	245	250	255
163 Ile Gln Glu Ser Val Lys Asp Arg Val Ile Asp Ser Arg Leu Gln Leu	260	265	270
164			
166 Phe Ile Thr Lys Pro Gly Leu Tyr Thr Cys Ile Ala Thr Asn Lys His	275	280	285
167			
169 Gly Glu Lys Phe Ser Thr Ala Lys Ala Ala Ala Thr Ile Ser Ile Ala	290	295	300
170			
172 Glu Trp Ser Lys Pro Gln Lys Asp Asn Lys Gly Tyr Cys Ala Gln Tyr	305	310	315
173			
175 Arg Gly Glu Val Cys Asn Ala Val Leu Ala Lys Asp Ala Leu Val Phe	325	330	335
176			
178 Leu Asn Thr Ser Tyr Ala Asp Pro Glu Glu Ala Gln Glu Leu Leu Val	340	345	350
179			
181 His Thr Ala Trp Asn Glu Leu Lys Val Val Ser Pro Val Cys Arg Pro	355	360	365
182			
184 Ala Ala Glu Ala Leu Leu Cys Asn His Ile Phe Gln Glu Cys Ser Pro	370	375	380
185			
187 Gly Val Val Pro Thr Pro Ile Pro Ile Cys Arg Glu Tyr Cys Leu Ala	385	390	395
188			
190 Val Lys Glu Leu Phe Cys Ala Lys Glu Trp Leu Val Met Glu Glu Lys	405	410	415
191			
193 Thr His Arg Gly Leu Tyr Arg Ser Glu Met His Leu Leu Ser Val Pro	420	425	430
194			
196 Lys Cys Ser Lys Leu Pro Ser Met His Trp Asp Pro Thr Ala Cys Ala	435	440	445
197			
199 Arg Leu Pro His Leu Asp Tyr Asn Lys Glu Asn Leu Lys Thr Phe Pro	450	455	460
200			
202 Pro Met Thr Ser Ser Lys Pro Ser Val Asp Ile Pro Asn Leu Pro Ser	465	470	475
203			
205 Ser Ser Ser Ser Phe Ser Val Ser Pro Thr Tyr Ser Met Thr Val	485	490	495
206			
208 Ile Ile Ser Ile Met Ser Ser Phe Ala Ile Phe Val Leu Leu Thr Ile	500	505	510
209			
211 Thr Thr Leu Tyr Cys Cys Arg Arg Lys Gln Trp Lys Asn Lys Lys	515	520	525
212			
214 Arg Glu Ser Ala Ala Val Thr Leu Thr Leu Pro Ser Glu Leu Leu	530	535	540
215			
217 Leu Asp Arg Leu His Pro Asn Pro Met Tyr Gln Arg Met Pro Leu Leu	545	550	555
218			
220 Leu Asn Pro Lys Leu Leu Ser Leu Glu Tyr Pro Arg Asn Asn Ile Glu	565	570	575
221			
223 Tyr Val Arg Asp Ile Gly Glu Gly Ala Phe Gly Arg Val Phe Gln Ala	580	585	590
224			
226 Arg Ala Pro Gly Leu Leu Pro Tyr Glu Pro Phe Thr Met Val Ala Val	595	600	605
227			
229 Lys Met Leu Lys Glu Glu Ala Ser Ala Asp Met Gln Ala Asp Phe Gln	610	615	620
230			
232 Arg Glu Ala Ala Leu Met Ala Glu Phe Asp Asn Pro Asn Ile Val Lys	625	630	635
233			

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235 Leu Leu Gly Val Cys Ala Val Gly Lys Pro Met Cys Leu Leu Phe Glu
236           645           650           655
238 Tyr Met Ala Tyr Gly Asp Leu Asn Glu Phe Leu Arg Ser Met Ser Pro
239           660           665           670
241 His Thr Val Cys Ser Leu Ser His Ser Asp Leu Ser Met Arg Ala Gln
242           675           680           685
244 Val Ser Ser Pro Gly Pro Pro Leu Ser Cys Ala Glu Gln Leu Cys
245           690           695           700
247 Ile Ala Arg Gln Val Ala Ala Gly Met Ala Tyr Leu Ser Glu Arg Lys
248   705           710           715           720
250 Phe Val His Arg Asp Leu Ala Thr Arg Asn Cys Leu Val Gly Glu Asn
251           725           730           735
253 Met Val Val Lys Ile Ala Asp Phe Gly Leu Ser Arg Asn Ile Tyr Ser
254           740           745           750
256 Ala Asp Tyr Tyr Lys Ala Asn Glu Asn Asp Ala Ile Pro Ile Arg Trp
257           755           760           765
259 Met Pro Pro Glu Ser Ile Phe Tyr Asn Arg Tyr Thr Thr Glu Ser Asp
260           770           775           780
262 Val Trp Ala Tyr Gly Val Val Leu Trp Glu Ile Phe Ser Tyr Gly Leu
263   785           790           795           800
265 Gln Pro Tyr Tyr Gly Met Ala His Glu Glu Val Ile Tyr Tyr Val Arg
266           805           810           815
268 Asp Gly Asn Ile Leu Ser Cys Pro Glu Asn Cys Pro Val Glu Leu Tyr
269           820           825           830
271 Asn Leu Met Arg Leu Cys Trp Ser Lys Leu Pro Ala Asp Arg Pro Ser
272           835           840           845
274 Phe Thr Ser Ile His Arg Ile Leu Glu Arg Met Cys Glu Arg Ala Glu
275           850           855           860
277 Gly Thr Val Ser Val
278   865
280 <210> SEQ ID NO: 3
281 <211> LENGTH: 20
282 <212> TYPE: DNA
283 <213> ORGANISM: homo sapiens
285 <400> SEQUENCE: 3
286 cagaaggaac ttgcgtcctgc
289 <210> SEQ ID NO: 4
290 <211> LENGTH: 20
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292 <213> ORGANISM: homo sapiens
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299 <211> LENGTH: 42
300 <212> TYPE: DNA
301 <213> ORGANISM: homo sapiens
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307 <210> SEQ ID NO: 6

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20

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316 <210> SEQ ID NO: 7 27
317 <211> LENGTH: 31
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343 <210> SEQ ID NO: 10
344 <211> LENGTH: 26
345 <212> TYPE: DNA
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349 ccagtcatgg agtatgttagg tgagac 26

VERIFICATION SUMMARY

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L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date